

**IN THE CLAIMS:**

Please amend claims 1-15 and 19 as follows:

1. (twice amended) A DNA analysis method for analyzing DNA polymorphism, comprising the steps of:
  - generating plural kinds of multiply-charged ions of a test DNA fragment by ionization, where each of the multiply-charged ions has five or more charges;
  - performing a mass spectrometry on the multiply-charged ions formed by the ionization so as to measure a mass spectrum of the test DNA fragment;
  - predicting possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on both an information about the number of each of four different nucleic acid bases that constitute the test DNA fragment and an information about a polymorphism point; and
  - comparing a plurality of the predicted mass spectrum patterns with the measured mass spectrum to determine a nucleic acid base on the polymorphism point.
2. (twice amended) The DNA analysis method according to claim 1, wherein the step of predicting includes predicting a mass-to-charge ratio ( $m/z$ ;  $m$  is an ion mass,  $z$  is a number of electric charges) of each of the plural kinds of multiply-charged ions in each of the two cases, and the step of comparing includes comparing the predicted mass-to-charge ratio ( $m/z$ ) of the predicted mass spectrum patterns with a mass-to-charge ratio ( $m/z$ ) of the measured mass spectrum.
3. (twice amended) The DNA analysis method according to claim 1, wherein the step of predicting includes predicting a mass-to-charge ratio ( $m/z$ ;  $m$  is

an ion mass,  $z$  is the number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio ( $m/z$ ) in each of the two cases, and the step of comparing includes comparing the predicted mass-to-charge ratio ( $m/z$ ) of the predicted mass spectrum patterns with a mass-to-charge ratio ( $m/z$ ) of the measured mass spectrum and compares the predicted relative ion intensities of the predicted mass spectrum patterns with relative ion intensities of the measured mass spectrum.

4. (twice amended) The DNA analysis method according to claim 1, further comprising the steps of:

sampling by supplying a sample including the test DNA fragment for the ionization intermittently at a predetermined time period; and

performing the following treatment to obtain  $S(i)$  for the measured mass spectrum ( $I(i)$ ) at an ordinal number " $i$ ",

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein  $m$  represents a predetermined natural number and  $w(n)$  represents a factor for the measured mass spectrum of the sample measured at  $n$ -th before the measurement of the sample which is measured at  $i$ -th; and

wherein the  $S(i)$  is compared with each of the predicted mass spectrum patterns.

5. (amended) The DNA analysis method according to claim 1, wherein the step of generating multiply-charged ions of the test DNA fragment by the ionization uses an air atomization.

6. (amended) The DNA analysis method according to claim 1, wherein a nucleic acid base of a single nucleotide polymorphism point in the test DNA fragment is specified.

7. (amended) The DNA analysis method according to claim 4, further comprising the step of:

displaying the occurrence of an emergency when a maximum ion intensity detected by the mass spectrometry is smaller than a predetermined threshold.

8. (twice amended) The DNA analysis method according to claim 7, further comprising the steps of:

generating information about the occurrence of the emergency .

9. (twice amended) The DNA analysis method according to claim 4, wherein the step of sampling introduces a standard sample for the ionization when a maximum ion intensity of the measured mass spectrum by the mass spectrometry is smaller than a predetermined threshold.

10. (twice amended) The DNA analysis method according to claim 9, wherein when a maximum ion intensity of a mass spectrum of the standard sample detected by the mass spectrometry is equal to or higher than the predetermined threshold, the sample where the maximum ion intensity of the mass spectrum is detected as one smaller than the predetermined threshold is re-supplied to the ionization by the sampling.

11. (twice amended) The DNA analysis method according to claim 9, further comprising the steps of:

utilizing a plurality of measurement systems, where each of the measurement systems comprises the steps of sampling, ionization, and mass spectrometry,

wherein when a maximum ion intensity of a mass spectrum of the standard sample detected by mass spectrometry in one measurement system of the plurality

of measurement systems is smaller than the predetermined threshold, the sample where a maximum ion intensity of a mass spectrum is detected as one smaller than the predetermined threshold at the one measurement system is transmitted for sampling of another measurement system except the one measurement system.

12. (twice amended) The DNA analysis method according to claim 9, further comprising the steps of:

utilizing a plurality of measurement systems, where each of the measurement systems comprises the steps of sampling, ionization, and mass spectrometry,

wherein when a maximum ion intensity of a mass spectrum of the standard sample detected by mass spectrometry in one measurement system of the plurality of measurement systems is smaller than the predetermined threshold, a sample intended to be measured by the one measurement system is sent for sampling of another measurement system except the one measurement system.

13. (amended) A DNA analysis method for analyzing DNA polymorphism, comprising the steps of:

sampling by supplying a sample including a test DNA fragment for ionization intermittently at a predetermined time period;

generating plural kinds of multiply-charged ions of the test DNA fragment by ionization, where each of the multiply-charged ions has five or more charges;

for performing a mass spectrometry on the multiply-charged ions formed by the ionization so as to measure a mass spectrum of the test DNA fragment;

performing the following treatment to obtain  $S(i)$  for the measured mass spectrum  $I(i)$  at an ordinal number "i",

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein  $m$  represents a predetermined natural number and  $w(n)$  represents a factor for the measured mass spectrum of the sample measured at  $n$ -th before the

measurement of the sample which is measured at i-th;

predicting possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on both an information about the number of each of four different nucleic acid bases that constitute the test DNA fragment and an information about a polymorphism point, wherein the step of predicting includes predicting a mass-to-charge ratio ( $m/z$ ;  $m$  is an ion mass,  $z$  is a number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio ( $m/z$ ) in each of the two cases; and

comparing a plurality of the predicted mass spectrum patterns with the measured mass spectrum to determine a nucleic acid base on the polymorphism point, wherein the step of comparing includes comparing the predicted mass-to-charge ratio ( $m/z$ ) of the predicted mass spectrum patterns with a mass-to-charge ratio ( $m/z$ ) of the measured mass spectrum and compares the predicted relative ion intensities of the predicted mass spectrum patterns with relative ion intensities of the measured mass spectrum, and wherein the  $S(i)$  is compared with each of the predicted mass spectrum patterns.

14. (amended) A DNA analysis method for analyzing DNA polymorphism, comprising the steps of:

sampling by supplying a sample including a test DNA fragment for ionization intermittently at a predetermined time period;

generating plural kinds of multiply-charged ions of the test DNA fragment ionization, where each of the multiply-charged ions has five or more charges;

performing a mass spectrometry on the multiply-charged ions formed by the ionization so as to measure a mass spectrum of the test DNA fragment;

performing the following treatment to obtain  $S(i)$  for the measured mass

spectrum ( $I(i)$ ) at an ordinal number “i”,

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein  $m$  represents a predetermined natural number and  $w(n)$  represents a factor for the measured mass spectrum of the sample measured at  $n$ -th before the measurement of the sample which is measured at  $i$ -th;

predicting possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and an other of the two cases is that the test DNA fragment is not polymorphic, based on both an information about the number of each of four different nucleic acid bases that constitute the test DNA fragment and an information about a polymorphism point, wherein step of predicting includes predicting a mass-to-charge ratio ( $m/z$ ;  $m$  is an ion mass,  $z$  is a number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio ( $m/z$ ) in each of the two cases; and

comparing including calculating a total ion intensity of each of the predicted mass spectrum patterns with respect to a plurality of peaks in the range of a predetermined mass-to-charge ratio ( $m/z$ ) and for selecting the predicted mass spectrum pattern which has a highest total ion intensity and comparing the predicted mass spectrum patterns having the highest total ion intensity with the measured mass spectrum to determine a nucleic acid base on the polymorphism point, and wherein the  $S(i)$  is compared with the selected predicted mass spectrum patterns.

15. (amended) A DNA analysis method for analyzing DNA polymorphism, comprising:

sampling by supplying a sample including a test DNA fragment for ionization intermittently at a predetermined time period;

generating plural kinds of multiply-charged ions of the test DNA fragment by ionization, where each of the multiply-charged ions has five or more charges;

performing a mass spectrometry on the multiply-charged ions formed by the ionization so as to measure a mass spectrum of the test DNA fragment;

performing the following treatment to obtain  $S(i)$  for the measured mass spectrum ( $I(i)$ ) at an ordinal number “i”,

$$S(i) = I(i) - \sum_{n=1}^m w(n)I(i-n)$$

wherein  $m$  represents a predetermined natural number and  $w(n)$  represents a factor for the measured mass spectrum of the sample measured at  $n$ -th before the measurement of the sample which is measured at  $i$ -th;

predicting possible mass spectrum patterns in each of two cases, where one of the two cases is that the test DNA fragment is polymorphic and the other is that the test DNA fragment is not polymorphic, based on both an information about the number of each of four different nucleic acid bases that constitutes the test DNA fragment and an information about a polymorphism point, wherein the step of predicting includes predicting a mass-to-charge ratio ( $m/z$ ;  $m$  is an ion mass,  $z$  is a number of electric charges) of each of the plural kinds of multiply-charged ions and a relative ion intensity corresponding to the mass-to-charge ratio ( $m/z$ ) in each of the two cases; and

comparing a plurality of the predicted mass spectrum patterns with the measured mass spectrum to determine a nucleic acid base on the polymorphism point, wherein the step of comparing includes selecting the predicted mass spectrum pattern such that a sum of a square root of a difference between a relative intensity of the measured mass spectrum having the  $S(i)$  and a relative intensity of the predicted mass spectrum pattern is smallest.

19. (amended) The DNA analysis method according claim 16, wherein the steps of generating, performing and selecting are subsequently repeated, the measured mass spectrum pattern ( $I(i)$ ) at an ordinal number “i” is subjected to the following treatment to obtain  $S(i)$ , and then the  $S(i)$  is compared with each of the